IN THE SPECIFICATION:

Please ADD the following paragraphs beginning at page 60, line 31 (which would be numbered sequentially from [0318] to [0325] to follow paragraph numbering in the published application):

[0318]   In one embodiment, the method of the present invention is a method of analyzing sequences of atomic groups including a first sequence having m atomic groups and a second sequence having n atomic groups where m and n are integers, comprising: a) preparing an array S[i] having array elements S[0] to S[m]; b) initializing all array elements of the array S[i] to zero and initializing an integer j to 1; c) adding 1 to each array element S[i] that is equal to an array element S[r] and that i ≥ r if the array element S[r] is equal to an array element S[r.times.1] where r is an occurrence position of j-th atomic group of the second sequence in the first sequence; d) adding 1 to the integer j; e) repeating the step c) and d) until the integer j exceeds n; and f) obtaining a longest common atomic group number between the first and the second sequences from a value of the array element S[m]. The method may further comprise: g) preparing an array data[k] having array elements data[0], data[1] . . . ; h) storing paired data (r, j) in an array element data[k] if the array element S[i] is changed in the step c) where k=S[r]; i) linking the paired data (r, j) stored in the step h) to paired data (r', j') if r'<r and j'<j where the paired data (r', j') is one stored in an array element data[k-1]; and j) obtaining a longest common subsequence between the first and the second sequences and occurrence positions of the longest common subsequence in the first and the second sequence by tracing the link formed in the step i). In addition, the method may further comprise: k) evaluating homology between the first and the second sequences based on the longest common atomic group number and a value of one of m and n, which may further comprise 1) searching for a sequence that is homologous with the first sequence from among a plurality of sequences, by successively assigning one of the plurality of sequences to the second sequence and executing the steps a) to f) and k).

[0319]   In an embodiment, the method of the present invention is a method of analyzing three-dimensional structures including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set, comprising: a) generating a combination of correspondence satisfying a restriction condition between the elements belonging to the first point set and the elements belonging to the second point set from among all candidates for the combination of correspondence; and b) calculating a root means square

distance between the elements corresponding in the combination of correspondence generated in the step a). The restriction condition may include order relation of the elements in the first and the second point sets that are ordered and/or proximity in a geometric relationship among a plurality of elements close to each other. The restriction condition may include a condition such that a candidate for the combination of correspondence satisfies a threshold value condition. The restriction condition may include a condition such that an attribute value of each of the elements belonging to the first point set coincides with an attribute value of the corresponding element belonging to the second point set in a candidate for the combination of correspondence.

[0320]   In an embodiment, the method of the present invention is a method of analyzing three-dimensional structures including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set, comprising: a) dividing the second point set into a plurality of subsets having a size that is determined by the size of the first point set; b) generating a combination of correspondence satisfying a restriction condition between the elements belonging to the first point set and the elements belonging to each of the subsets of the second point set from among all candidates for the combination of correspondence; and c) calculating a root mean square distance between the elements corresponding in the combination of correspondence generated in the step b). The second point set may be divided into the subsets so that the number of elements belonging to each of the subsets is a function of the number of elements belonging to the first point set. The second point set may be divided into the subsets so that a spatial size of each of the subsets is nearly equal to a spatial size of the first point set.

[0321]   In an embodiment, the method of the present invention is a method of analyzing three-dimensional structures including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set, comprising: a) dividing the first point set and second point set into first subsets and second subsets, respectively, according to a secondary structure exhibited by the three-dimensional coordinates of the elements of the first and the second point sets; b) generating a combination of correspondence satisfying a first restriction condition between the first subsets and the second subsets from among candidates for the combination of correspondence; c) determining an optimum correspondence between the elements belonging to each pair of subsets corresponding in the combination of correspondence

generated in the step b), and d) calculating a root mean square distance between all of the elements corresponding in the optimum correspondence in the step c). The optimum correspondence determining step may comprise the substeps of: i) generating a combination of correspondence satisfying a second restriction condition between the elements belonging to the subsets corresponding in the combination of the correspondence generated in the step b); ii) calculating a root mean square distance between the elements corresponding in the combination of the correspondence generated in the substep i); iii) selecting a combination of the correspondence as the optimum correspondence according to the value of the root mean square distance value calculated in the substep ii).

[0322]   In an embodiment, the apparatus of the present invention is an apparatus for analyzing sequences of atomic groups including a first sequence having m atomic groups and a second sequence having n atomic groups where m and n are integers, comprising: means for preparing an array S[i] having array elements S[0] to S[m]; means for initializing all array elements of the array S[i] to zero and initializing an integer j to 1; means for renewing the array S[i] by adding 1 to each array element S[i] that is equal to an array element S[r] and that $i \geq r$ if the array element S[r] is equal to an array element S[r-1] where r is an occurrence position of j-th atomic group of the second sequence in the first sequence; means for incrementing the integer j by 1; means for repeatedly activating the renewing means and the incrementing means until the integer j exceeds n; and means for obtaining a longest common atomic group number between the first and the second sequences from a value of the array element S[m]. The apparatus may further comprise: means for preparing an array data[k] having array elements data[0], data[1] . . . ; means for storing paired data (r, j) in an array element data [k] if the array element S[i] is changed by the renewing means where k=S[r]; means for linking the paired data (r, j) stored by the storing means to paired data (r', j') if r'<r and j'<j where the paired data (r', j') is one stored in an array element data [k-1]; and means for obtaining a longest common subsequence between the first and the second sequences and occurrence positions of the longest common subsequence in the first and the second sequence by tracing the link formed by the linking means. The apparatus may further comprise means for evaluating homology between the first and the second sequences based on the longest common atomic group number and a value of one of m and n.

[0323]   In an embodiment, the apparatus of the present invention is an apparatus for analyzing three-dimensional structures including a first structure expressed by three-dimensional

coordinates of elements belonging to a first point set and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set, comprising: means for generating a combination of correspondence satisfying a restriction condition between the elements belonging to the first point set and the elements belonging to the second point set from among all candidates for the combination of correspondence; and means for calculating a root mean square distance between the elements corresponding in the combination of correspondence generated by the generating means.

[0324]   In an embodiment, the apparatus of the present invention is an apparatus for analyzing three-dimensional structures including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set, comprising: means for dividing the second point set into a plurality of subsets having a size that is determined by the size of the first point set; means for generating a combination of correspondence satisfying a restriction condition between the elements belonging to the first point set and the elements belonging to each of the subsets of the second point set from among all candidates for the combination of correspondence; and means for calculating a root mean square distance between the elements corresponding in the combination of correspondence generated by the generating means.

[0325]   In an embodiment, the apparatus of the present invention is an apparatus for analyzing three-dimensional structures including a first structure expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure expressed by three-dimensional coordinates of elements belonging to a second point set, comprising: means for dividing the first point set and the second point set into first subsets and second subsets, respectively, according to a secondary structure exhibited by the three-dimensional coordinates of the elements of the first and the second point sets; means for generating a combination of correspondence satisfying a first restriction condition between the first subsets and the second subsets from among candidates for the combination of correspondence; means for determining an optimum correspondence between the elements belonging to each pair of subsets corresponding in the combination of correspondence generated in the generating means, and means for calculating a root mean square distance between all of the elements corresponding in the optimum correspondence.